

DATE: 04/03/2000
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This Raw Listing contains the General Information Section and up to first 5 pages.

ENTERED

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1 <110> APPLICANT: Greene, John M.
2 Fleischmann, Robert D.
3 Ni, Jian
4 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Genes
5 <130> FILE REFERENCE: 1488.0710005
6 <140> CURRENT APPLICATION NUMBER: US/09/526,437
7 <141> CURRENT FILING DATE: 2000-03-15
8 <160> NUMBER OF SEQ ID NOS: 11
9 <170> SOFTWARE: PatentIn Ver. 2.0
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28 Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr
29 -15 -10 -5
30 cag gaa acg ttt cct cca aag tac ctt cat tat gac gaa gaa acc tct 153
31 Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser
32 -1 1 5 10 15
33 cat cag ctg ttg tgt gac aaa tgt cct cct ggt acc tac cta aaa caa 201
34 His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln
35 20 25 30
36 cac tgt aca gca aag tgg aag acc gtg tgc gcc cct tgc cct gac cac 249
37 His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His
38 35 40 45
39 tac tac aca gac agc tgg cac acc agt gac gag tgt cta tac tgc agc 297
40 Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser
41 50 55 60
42 ccc gtg tgc aag gag ctg cag tac gtc aag cag gag tgc aat cgc acc 345
43 Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr
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51	gct gga acc cca gag cga aat aca gtt tgc aaa aga tgt cca gat ggg	489
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88	Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp	
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91	Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His	
92	320 325 330 335	
93	ttt ccc aaa act gtc act cag agt cta aag aag acc atc agg ttc ctt	1161
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103  aggcacttga ggctttcagt gatatctttc tcattaccag tgactaattt tgccacaggg 1378
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118  Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
119          30          35          40
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121          45          50          55
122  Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
123          60          65          70          75
124  Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
125          80          85          90
126  Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
127          95          100          105
128  Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
129          110          115          120
130  Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
131          125          130          135
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133          140          145          150          155
134  Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
135          160          165          170
136  Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
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138  Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
139          190          195          200
140  Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
141          205          210          215
142  Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
143          220          225          230          235
144  Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln

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149          270          275          280
150      Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
151          285          290          295
152      Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
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184      gaa gaa acc tct cat cag ctg ttg tgt gac aaa tgt cct cct ggt acc      144
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186          15          20          25
187      tac cta aaa caa cac tgt aca gca aag tgg aag acc gtg tgc gcc cct      192
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190      tgc cct gac cac tac tac aca gac agc tgg cac acc agt gac gag tgt      240
191      Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
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194      Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu

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200	Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe				
201	95	100	105		
202	gga gtg gtg caa gct gga acc cca gag cga aat aca gtt tgc aaa aga	432			
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208	aga aaa cac aca aat tgc agt gtc ttt ggt ctc ctg cta act cag aaa	528			
209	Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys				
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211	gga aat gca aca cac gac aac ata tgt tcc gga aac agt gaa tca act	576			
212	Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr				
213	160	165	170		
214	caa aaa tgt gga ata gat gtt acc ctg tgt gag gag gca ttc ttc agg	624			
215	Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg				
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218	Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val				
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220	gac aat ttg cct ggc acc aaa gta aac gca gag agt gta gag agg ata	720			
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223	aaa cgg caa cac agc tca caa gaa cag act ttc cag ctg ctg aag tta	768			
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236	Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys				
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238	ccc agt gac cag atc ctg aag ctg ctc agt ttg tgg cga ata aaa aat	1008			
239	Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn				
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242	Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser				
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VERIFICATION SUMMARY
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Line ? Error/Warning

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